



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102297

**TO: Phillip Gabel
Location: 8b03 / 9e12
Tuesday, August 26, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 454651**

**From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498**

jan.delaval@uspto.gov

Search Notes

10229X

Deval, Jan

From: Gambel, Phillip
Sent: Tuesday, August 26, 2003 9:27 AM
To: Delaval, Jan
Subject: 09 / 454,651 ifw amd

jan

please perform a sequence and a sequence interference search for

ussn 09/ 454,651 (ifw amd)

SEQ ID NO: 23

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
 Art Unit _____ Phone Number 30 _____ Serial Number _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STN 1000
 1000 University & Chemical Library
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STAFF USE ONLY

Searcher _____
 Searcher Phone # _____

Searcher Location _____

Date Searcher Picked _____

Date Time slot _____

Searcher Prep & Review Time _____

Client Prep Time _____

Waiting Time _____

Type of Search

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

Bibliographic _____

Litigation _____

Full text _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel Orbit _____

Web of Science _____

Sequence Systems ☒

Web of Invention _____

Chemical Abstracts _____

Other _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:18:32 ; Search time 39 Seconds
(without alignments)

532.627 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKEVKEVA.....LRVQNTFNWNTTQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	A45803	B-cell-restricted
2	1085	94.4	289	G00031	B7 protein - red-c
3	738	64.2	299	I46690	CD80 precursor - r
4	601.5	52.3	321	I54766	B-lymphocyte activ
5	561	48.8	309	I49503	B-lymphocyte activ
6	185	16.1	275	JC7604	CD86 spliced varia
7	182	15.8	329	I448754	B7-2 antigen - hum
8	152	13.2	309	I49522	gene B7-2 protein
9	140.5	12.2	330	I46691	CD86 precursor - r
10	133.5	11.6	583	I39428	alcam - human
11	129	11.2	221	Q0BB48	BARF1 protein - hu
12	127	11.1	526	J70587	butyrophilin precu
13	122.5	10.7	588	JH0506	adhesion molecule
14	122.5	10.7	588	A45254	surface glycoprote
15	120.5	10.5	509	JC5288	SHP substrate-1 pr
16	120.5	10.5	513	JC5289	SHP substrate-1 pr
17	118	10.3	487	S65133	butyrophilin - mou
18	116.5	10.1	1088	IJXLNL	neural cell adhesi
19	115	10.0	761	IJHUNG	neural cell adhesi
20	112.5	9.8	725	JE0099	neural cell adhesi
21	110.5	9.6	587	JH0464	DM-GRASP precursor
22	109.5	9.5	646	I38049	cell surface glyco
23	109.5	9.5	853	IJBONC	neural cell adhesi
24	109	9.5	526	A37821	butyrophilin - bov
25	109	9.5	2029	1 TDFILK	protein-tyrosine-p
26	108	9.4	871	I48696	protein-tyrosine k
27	108	9.4	881	I48697	protein-tyrosine k
28	107.5	9.4	5175	I20992	hypothetical prote
29	107.5	9.4	5198	I43290	hemiscentin precurs

30 106.5 9.3 333 2 A31923
31 106.5 9.3 858 1 IJRTNC
32 106 9.2 267 2 PJ0064
33 105.5 9.2 1091 1 IJCHNL
34 104.5 9.1 210 2 A56169
35 104 9.1 307 1 RWM5BC
36 104 9.1 725 2 JE0100
37 104 9.1 1092 1 JN0635
38 103.5 9.0 480 2 A56182
39 103.5 9.0 725 1 IJMSNG
40 103.5 9.0 1115 1 IJMSNL
41 103 9.0 423 2 T29549
42 103 9.0 1273 2 T42405
43 102.5 8.9 503 2 JC5287
44 102 8.9 1443 2 I50600
45 101 8.8 1033 2 S19247

ALIGNMENTS

RESULT 1

A45803

B-cell-restricted antigen B7 precursor - human

N:Alternate names: B-lymphocyte activation antigen B7

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999

C:Accession: I54495; A45803

R:Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

Immunogenetics 36, 175-181, 1992

A:Title: Genomic organization and chromosomal location of the human gene encoding the B-1

A:Reference number: I54495; MUID:92307753; PMID:1377173

A:Accession: I54495

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-288 <RES>

A:Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329

R:Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.

J. Immunol. 143, 2714-2722, 1989

A:Title: B7, a new member of the Ig superfamily with unique expression on activated and i

A:Reference number: A45803; MUID:90010147; PMID:2794510

A:Accession: A45803

A:Molecule type: mRNA

A:Residues: 1-288 <FRE>

A:Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916

C:Genetics:

A:Gene: GDB:CD80; CD28LGL1; CD28

A:Cross-references: GDB:251792; OMIM:112203

A:Map position: 3q13.3-3q21

A:Introns: 34/1; 140/1; 234/1; 266/1

C:Superfamily: B-lymphocyte restricted antigen B7

C:Keywords: transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1149; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 1.8e-85;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVWQEKVVLTMWSDGMNIWPE 60
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVWQEKVVLTMWSDGMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVSKADFTPTS 120
Db 87 YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVSKADFTPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
QY 181 NMTTNSFWCLIKYGLRVNQTNNNTTQEHFPDN 216

```
Db 207 MMTNHSFMCLIKYGLRLVQNTFNWNTTKQEHFPDN 242

RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C>Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G00031
A:Accession: G00031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <VIL>
A:Cross-references: EMBL:U19833; NID:G644783; PIDN:AAA86700.1; PID:G644784
C:Genetics:
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 94.4%; Score 1085; DB 2; Length 289;
Best Local Similarity 95.3%; Pred. No. 2.7e-80;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDMNIWPEY 61
DB 28 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDMNIWPEY 87
QY 62 KNRITFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTSI 121
DB 88 KNRITFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTSI 147
QY 122 SDFEIPNTNIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELVAVSKLDNF 181
DB 148 TDFEIPNTNIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELVAVSKLDNF 207
QY 182 MTTNHSFMCLIKYGLRLVQNTFNWNTTKQEHFPDN 216
DB 208 MTTNHSFMCLIKYGLRLVQNTFNWNTTKQEHFPDN 242

RESULT 3
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849; PMID:7642234
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:G755096; PIDN:BAA08643.1; PID:G755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 64.2%; Score 738; DB 2; Length 299;
Best Local Similarity 63.9%; Pred. No. 3e-52;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY 4 HFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDMNIWPEYKN 63
DB 29 HFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDMNIWPEYKN 88
QY 64 RTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTSI 123
DB 89 RTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTSI 148
QY 124 RTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTSI 183
DB 148 RTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTSI 207

us-09-454-651b-23.rpr

Db 149 IGHDPNVKIRCSASGGFPPEPLANWDEELNAVNTTVDQLDTELYSVSSELDNFNT 208
QY 184 TNHSPMCLIKYGLRLVQNTFNWNTTKQEHFPDN 211
DB 209 NNHSIVCLIKYGLSVSQIFPWSKPKQEHFPDN 236

RESULT 4
I54766
B-lymphocyte activation antigen 7-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: I54766
R:Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A:Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and functional
A:Reference number: I54766; MUID:95252184; PMID:7537533
A:Accession: I54766
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-321 <RES>
A:Cross-references: EMBL:U05593; NID:G453381; PIDN:AAA80154.1; PID:G453382
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 52.3%; Score 601.5; DB 2; Length 321;
Best Local Similarity 54.4%; Pred. No. 3.4e-41;
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDMNIWPEY 59
DB 31 GLSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDMNIWPEY 90
QY 60 EYKNTTPTDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPT 119
DB 91 EYKNTTPTDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPT 150
QY 120 SISDFEIPNTNIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELVAVSKLD 179
DB 151 NITEYGNPSADIKRITCFASGGFPKPLSLWLENGEELNAINTVSQDPETELVAVSKLD 210
QY 180 PMTNTNHSFMCLIKYGLRLVQNTFNWNTTKQEHFPDN 205
DB 211 PMTNTNHSFMCLIKYGLRLVQNTFNWNTTKQEHFPDN 236

RESULT 5
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789; PMID:7686531
A:Accession: I49503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L12589; NID:G293299; PIDN:AAA37240.1; PID:G293301
R:Freeman, G.J.; Gray, G.S.; Gimmi, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fingerot,
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homologue
A:Reference number: S17291; MUID:91341422; PMID:1714935
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <PRE>
A:Cross-references: EMBL:X60958; NID:G50111; PIDN:CAA43291.1; PID:G50112
R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
A:Reference number: I49521; MUID:94220123; PMID:7513163
```

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:17:12 ; Search time 23 Seconds

(without alignments)
441.642 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVHVTKEVKEVA.....LRVNQTFNWNNTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1	CD80 HUMAN
2	738	64.2	299	1	CD80 RABBIT
3	561	48.8	306	1	CD80 MOUSE
4	182	15.8	329	1	CD86 HUMAN
5	161	14.0	302	1	ICOL HUMAN
6	152	13.2	309	1	CD86 MOUSE
7	150.5	13.1	322	1	ICOL MOUSE
8	140.5	12.2	330	1	CD86 RABBIT
9	138	12.0	509	1	SHS1 RAT
10	134.5	11.7	583	1	C166 MOUSE
11	133.5	11.6	583	1	C166 HUMAN
12	129	11.2	221	1	BRF1 EBV
13	127	11.1	526	1	BUTY HUMAN
14	122.5	10.7	588	1	C166 CHICK
15	120.5	10.5	513	1	SHS1 MOUSE
16	120	10.4	506	1	SHS1 BOVIN
17	119	10.4	524	1	BUTY MOUSE
18	116.5	10.1	1088	1	NCA1 XENLA
19	115	10.0	761	1	NCA2 HUMAN
20	115	10.0	848	1	NCA1 HUMAN
21	110.5	9.6	321	1	TCB FLV
22	110	9.6	398	1	SRB1 HUMAN
23	109.5	9.5	646	1	MU18 HUMAN
24	109.5	9.5	853	1	NCA1 BOVIN
25	109	9.5	387	1	SRB2 HUMAN
26	109	9.5	526	1	BUTY BOVIN
27	109	9.5	2029	1	LAR DROME
28	108.5	9.4	365	1	AMAL DROME
29	107.5	9.4	333	1	AMAL MOUSE
30	106.5	9.3	858	1	NCA1 RAT
31	105	9.1	319	1	A33 HUMAN
32	105	9.1	1091	1	NCA1 CHICK
33	104	9.1	1092	1	NCA2 XENLA

34	103.5	9.0	725	1	NCA2 MOUSE
35	103.5	9.0	1115	1	NCA1 MOUSE
36	103	9.0	298	1	JAM2 HUMAN
37	102.5	8.9	503	1	SHS1 HUMAN
38	102	8.9	1443	1	NEOL CHICK
39	101.5	8.8	403	1	RAGE MOUSE
40	100	8.7	413	1	HEMO MANSE
41	99.5	8.7	1338	1	VGR1 HUMAN
42	98.5	8.6	365	1	CXAR HUMAN
43	98.5	8.6	1242	1	NBNH MOUSE
44	98	8.5	278	1	OK2G RAT
45	98	8.5	298	1	JAM1 BOVIN

P13594	mus musculus
P13595	mus musculus
P57087	homo sapien
P78324	h protei-t
Q0610	gallus gall
Q62151	mus musculus
P31398	manduca sex
P17948	h vascular
P78310	homo sapien
Q9QZS7	mus musculus
P04218	rattus norv
Q9XL56	bos taurus

ALIGNMENTS

RESULT 1	
CD80 HUMAN	
ID	CD80 HUMAN STANDARD; PRT; 288 AA.
AC	P33681;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
DE	antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN	CD80 OR CD28LG1 OR CD28LG OR IAB7.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lymphoid;
RX	MEDLINE=90010147; PubMed=2794510;
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,
RA	Nadler L.M.;
RT	"B7, a new member of the Ig superfamily with unique expression on
RT	activated and neoplastic B cells.,"
RL	J. Immunol. 143:2714-2722(1989).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92307753; PubMed=1377173;
RA	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
RA	Dupont B.;
RT	"Genomic organization and chromosomal location of the human gene
RT	encoding the B-lymphocyte activation antigen B7.,"
RL	Immunogenetics 36:175-181(1992).
RN	[3]
RP	SEQUENCE OF 35-38.
RX	MEDLINE=91341422; PubMed=1714935;
RA	Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
RA	White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT	"Structure, expression, and T cell costimulatory activity of the
RT	murine homologue of the human B lymphocyte activation antigen B7.,"
RL	J. Exp. Med. 174:625-631(1991).
RN	[4]
RP	CHARACTERIZATION.
RX	MEDLINE=95088403; PubMed=7527824;
RA	Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA	Okumura K., Ito D., Azuma M.;
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT	cell proliferation, cytokine production, and generation of CTL.,"
RL	J. Immunol. 154:97-105(1995).
RN	[5]
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX	MEDLINE=20125021; PubMed=10661405;
RA	Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
RA	Jones E.V., Stuart D.I., Davis S.J.;
RT	"Structure and dimerization of a soluble form of B7-1.,"
RL	Immunity 12:51-60(2000).
CC	!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC	LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE

CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
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 CC -----
 CC EMBL; M27533; AAA36045.1; -;
 CC EMBL; M83077; AAA58390.1; -;
 CC EMBL; M83072; AAA58390.1; JOINED.
 CC EMBL; M83073; AAA58390.1; JOINED.
 CC EMBL; M83074; AAA58390.1; JOINED.
 CC PIR; I54495; A45803.
 CC PDB; 1DR9; 10-JAN-01.
 CC PDB; 1I8L; 04-APR-01.
 CC Genew; HGNC:1700; CD80.
 CC MIM; 112203; -;
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00403; Ig; 1.
 CC PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor; 3D-structure.
 FT SIGNAL 1 34
 FT CHAIN 35 298 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
 FT DOMAIN 35 242 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 243 263 POTENTIAL.
 FT DOMAIN 264 288 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 35 135 IG-LIKE V-TYPE.
 FT DOMAIN 145 230 IG-LIKE C2-TYPE.
 FT DISULFID 50 116
 FT DISULFID 162 216
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT STRAND 37 41
 FT TURN 42 43
 FT STRAND 46 48
 FT TURN 56 57
 FT TURN 58 61
 FT HELIX 58 61
 FT STRAND 63 68
 FT TURN 69 70
 FT STRAND 71 77
 FT TURN 78 79
 FT STRAND 80 83
 FT STRAND 85 88
 FT HELIX 85 88
 FT TURN 89 90
 FT STRAND 91 94
 FT TURN 96 99
 FT STRAND 100 103
 FT STRAND 108 110
 FT HELIX 108 110
 FT STRAND 112 120
 FT TURN 123 124
 FT TURN 127 139
 FT STRAND 146 151

FT TURN 155 156
 FT STRAND 157 167
 FT STRAND 171 177
 FT STRAND 181 182
 FT STRAND 186 191
 FT TURN 193 195
 FT STRAND 198 207
 FT TURN 208 209
 FT STRAND 212 220
 FT TURN 221 222
 FT STRAND 225 231
 SQ SEQUENCE 288 AA; 33048 MW; BAA53EE34528B1E4 CRC64;
 Query Match 100.0%; Score 1149; DB 1; Length 288;
 Best Local Similarity 100.0%; Pred. NO. 1.7e-98;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCSGVHVTKEVKEVATLSGHNVSVEELAQTRIYQKQKMKVLTMMSGDMNIWPE 60
 DB 27 GLSHFCSGVHVTKEVKEVATLSGHNVSVEELAQTRIYQKQKMKVLTMMSGDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLYKEDAFKREHLAEVTLVKADFPPTPS 120
 DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLYKEDAFKREHLAEVTLVKADFPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGELNAINITVSQDPETELYAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGELNAINITVSQDPETELYAVSSKLD 206
 QY 181 NMTNHSFMCILIKYGHRLRVNQTFNWTTKQEHFPDN 216
 DB 207 NMTNHSFMCILIKYGHRLRVNQTFNWTTKQEHFPDN 242
 RESULT 2
 CD80 RABIT STANDARD; PRT; 299 AA.
 ID AC P42070;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE T lymphocyte activation antigen CD80 precursor (Activation E7-1
 DE antigen).
 OS CD80.
 GN Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB:HM;
 RC MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; D49843; BAA08643.1; -;

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:17:57 ; Search time 96 Seconds

(without alignments)
580.618 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCGVHVTKEVKEVA.....LRVNTFNWNTKQEHFFDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1118	97.3	288	6	O77684 macaca neme
2	1100	95.7	288	6	Q28499 macaca mula
3	1085	94.4	288	6	Q9BDN6 cercocebus
4	1085	94.4	289	6	Q28347 cercocebus
5	772	67.2	296	6	Q8WMZ2 sus scrofa
6	764	66.5	230	6	Q9N213 sus scrofa
7	762.5	66.4	288	6	Q9TT70 sus scrofa
8	762.5	66.4	297	6	Q9BE99 sus scrofa
9	761	66.2	229	6	Q9TT71 sus scrofa
10	743	64.7	292	6	Q9GMZ8 felis silve
11	743	64.7	292	6	O02758 felis silve
12	719	62.6	304	6	Q9TQX1 canis fami
13	717.5	62.4	296	6	O46405 bos taurus
14	705	61.4	235	6	Q9N0T0 canis fami
15	705	61.4	235	6	O9TQ88 canis fami
16	659	57.4	294	11	Q8BH36 mesocricetu

17	603.5	52.5	321	11	O35187	O35187 rattus norv
18	602	52.4	290	11	Q62680	Q62680 rattus norv
19	601.5	52.3	321	11	O62624	O62624 rattus norv
20	596	51.9	321	11	O55202	O55202 rattus norv
21	560	48.7	306	11	Q9RI29	Q9RI29 mus musculu
22	350	30.5	174	6	Q9GMZ9	Q9gmz9 felis silve
23	349.5	30.4	173	6	Q9SL17	Q9sl17 felis silve
24	255.5	22.2	212	11	O61332	O61332 mus musculu
25	200.5	17.4	329	6	Q9XSX6	Q9xsx6 felis silve
26	200.5	17.4	332	6	Q9GMZ7	Q9gmz7 felis silve
27	200.5	17.4	332	6	Q9SL16	Q9sl16 felis silve
28	188.5	16.4	280	6	Q9TTF1	Q9ttf1 canis fami
29	188.5	16.4	296	13	O42404	O42404 gallus gall
30	182	15.8	329	6	Q9TTF2	Q9ttf2 canis fami
31	178	15.5	323	6	Q9BDM2	Q9bdm2 cercopithec
32	177	15.4	323	6	Q9BDM9	Q9bdm9 macaca neme
33	177	15.4	323	6	Q9BDM4	Q9bdm4 macaca mula
34	176	15.3	275	6	Q9BDN9	Q9bdn9 papio arubi
35	176	15.3	323	6	Q9BDB8	Q9bdb8 cercocebus
36	171	14.9	284	6	Q9GL33	Q9gl33 bos taurus
37	166.5	14.5	289	11	O8K3J3	O8k3j3 meriones un
38	165	14.4	281	11	O8CJ58	O8cje8 mesocricetu
39	162	14.1	313	11	O35531	O35531 rattus norv
40	161.5	14.1	325	6	O02838	O02838 sus scrofa
41	159	13.8	316	11	Q9VE98	Q9ve98 mus musculu
42	156.5	13.6	290	4	Q9NZQ7	Q9nzz7 homo sapien
43	153	13.3	290	11	Q9EP73	Q9ep73 mus musculu
44	153	13.3	356	11	O64381	O64381 mus musculu
45	152	13.2	314	11	Q61238	Q61238 mus musculu

ALIGNMENTS

RESULT 1

O77684
ID O77684 PRELIMINARY; PRT; 288 AA.
AC O77684;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein.
GN B7.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G., Hnatyszyn J.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079519; AAC31555.1; -
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF000047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 288 AA; 33131 MW; 76B8C42839E9AB79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;

Best Local Similarity 97.7%; Pred. No. 1e-92; Mismatches 4; Indels 0; Gaps 0;
Matches 210; Conservative 1;

Qy 2 LSHFCGVHVTKEVKEVATLSGHNVSVEELAQTRIYNQKXKVLTMWSDMNWPEY 61

Db 28 LSHFCGVHVTKEVKEVATLSGHNVSVEELAQTRIYNQKXKVLTMWSDMNWPEY 87

Qy 62 KNTIFDITNLSIVIALRPSDEGYECVULKYKDAFKREHLAEVTLVSKADFTPSI 121

Db 88 KNTIFDITNLSIVIALRPSDEGYECVULKYKDAFKREHLAEVTLVSKADFTPSI 147


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QY 122 SDFEPTSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPPSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCCLKYGLRVNQTFFNNTTKQEHFPDN 216
DB 208 MTNHSFMCCLKYGLRVNQTFFNNTTKQEHFPDN 242

RESULT 2
Q28499
ID Q28499 PRELIMINARY; PRT; 288 AA.
AC Q28499;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein (CD80 protein precursor).
GN B7 OR N939.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Wayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328 (2001).
DR EMBL; U19840; AAA86706.1; -.
DR EMBL; AF344849; AAK37609.1; -.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 26 POTENTIAL.
QY SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;
Best Local Similarity 96.3%; Pred. No. 4.2e-91;
Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYWQEKVMVLTWMSGDMNIWPEY 61
DB 28 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYWQEKVMVLTWMSGDMNIWPEY 87

QY 62 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPTPSI 121
DB 88 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPTPSI 147

QY 122 SDFEPTSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPPSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCCLKYGLRVNQTFFNNTTKQEHFPDN 216
DB 208 MTNHSFMCCLKYGLRVNQTFFNNTTKQEHFPDN 242

RESULT 4
Q28347
ID Q28347 PRELIMINARY; PRT; 289 AA.
AC Q28347;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein (Fragment).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Wayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and

```

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RESULT 3
Q28DN6
ID Q28DN6 PRELIMINARY; PRT; 288 AA.
AC Q28DN6;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE CD80 protein.
GN MNE71.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328 (2001).
DR EMBL; AF344839; AAK37535.1; -.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity 95.3%; Pred. No. 9.4e-90;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYWQEKVMVLTWMSGDMNIWPEY 61
DB 28 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYWQEKVMVLTWMSGDMNIWPEY 87

QY 62 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPTPSI 121
DB 88 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPTPSI 147

QY 122 SDFEPTSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPPSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCCLKYGLRVNQTFFNNTTKQEHFPDN 216
DB 208 MTNHSFMCCLKYGLRVNQTFFNNTTKQEHFPDN 242

RESULT 4
Q28347
ID Q28347 PRELIMINARY; PRT; 289 AA.
AC Q28347;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein (Fragment).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Wayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and

```

Accession	Gene	Protein	Accession	Gene	Protein
1	1149	100.0	288	16	AAK67989
2	1149	100.0	288	18	AAW38414
3	1149	100.0	288	20	AAW67804
4	1149	100.0	288	21	AAW37364
5	1149	100.0	288	21	AAE37087
6	1149	100.0	288	21	AAE99866
7	1149	100.0	288	21	AAE44289
8	1149	100.0	288	21	AAE59201
9	1149	100.0	288	22	AAU05121
10	1149	100.0	288	22	AAU05120

10	1149	100.0	288	22	AA5119955
11	1149	100.0	288	23	ABP68563
12	1149	100.0	288	23	ABF78363
13	1149	100.0	288	23	AA115800
14	1149	100.0	288	23	AGC32487
15	1149	100.0	288	23	AAE14633
16	1149	100.0	288	23	AA15829
17	1149	100.0	288	23	AA50795
18	1149	100.0	288	24	ABU07246
19	1149	100.0	288	24	ABU07247
20	1149	100.0	288	24	ABU07248
21	1149	100.0	288	24	ABU07249
22	1149	100.0	288	24	ABU07250
23	1149	100.0	288	24	ABU07251
24	1149	100.0	288	24	ABU07254
25	1149	100.0	288	24	ABU07255
26	1149	100.0	288	24	ABU07257
27	1149	100.0	288	24	ABU07260
28	1149	100.0	288	24	ABU07261
29	1149	100.0	288	24	ABU07265
30	1149	100.0	288	24	ABU07266
31	1149	100.0	288	24	ABU07267
32	1149	100.0	288	24	ABU07268
33	1149	100.0	288	24	ABU07269
34	1149	100.0	473	18	AAW41415
35	1146	99.7	251	20	AAW90208
36	1146	99.7	251	20	AAW07264
37	1144	99.6	475	18	AAW38415
38	1144	99.6	475	18	AAW07258
39	1143	99.5	488	20	AAW86004
40	1143	99.5	488	22	AAH83836
41	1143	99.5	488	24	ABU07253
42	1143	99.5	488	24	ABU07262
43	1143	99.5	492	19	AAW42338
44	1143	99.5	492	20	AAW07269
45	1148	99.0	480	20	AAW90206

B lymphocyte antigen; B7-1; B cell activation antigen; CD28; ligand; T cell surface antigen; transmembrane protein.

RESULT 2
AW38414
D A^{nc} Standard; Protein; 288 AA.

XX Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
 KW T-cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
 XX

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:23:43 ; Search time 57 Seconds
(without alignments)
500.065 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIHVTKEVKEVA.....LRVNQTFNNTTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCTUS_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1149	100.0	226	10	US-09-915-789A-21
2	1149	100.0	288	8	US-08-592-711-2
3	1149	100.0	288	9	US-09-772-102-14
4	1149	100.0	288	9	US-09-837-867A-19
5	1149	100.0	288	10	US-09-910-174A-5
6	1149	100.0	288	10	US-09-896-738-10
7	1149	100.0	288	10	US-09-915-789A-15
8	1149	100.0	288	11	US-09-962-969-19
9	1149	100.0	288	11	US-09-350-202-2
10	1149	100.0	288	12	US-10-032-214-278
11	1149	100.0	288	15	US-10-261-101-2
12	1149	100.0	473	10	US-09-910-059-131
13	1143	99.5	492	10	US-09-845-899A-3
14	1129	98.3	288	12	US-10-032-214-94
15	1121	97.6	288	12	US-10-032-214-69

16	1121	97.6	288	12	US-10-032-214-82	Sequence 82, Appl
17	1119	97.4	288	12	US-10-032-214-71	Sequence 71, Appl
18	1119	97.4	288	12	US-10-032-214-77	Sequence 77, Appl
19	1119	97.4	288	12	US-10-032-214-225	Sequence 225, Appl
20	1118	97.3	288	12	US-10-032-214-84	Sequence 84, Appl
21	1116	97.1	288	12	US-10-032-214-76	Sequence 76, Appl
22	1116	97.1	288	12	US-10-032-214-86	Sequence 86, Appl
23	1116	97.1	288	12	US-10-032-214-87	Sequence 87, Appl
24	1116	97.1	288	12	US-10-032-214-286	Sequence 286, Appl
25	1114	97.0	288	12	US-10-032-214-226	Sequence 226, Appl
26	1114	97.0	288	12	US-10-032-214-251	Sequence 251, Appl
27	1113	96.9	288	12	US-10-032-214-90	Sequence 90, Appl
28	1113	96.9	288	12	US-10-032-214-228	Sequence 228, Appl
29	1113	96.9	288	12	US-10-032-214-250	Sequence 250, Appl
30	1112	96.8	288	12	US-10-032-214-78	Sequence 78, Appl
31	1112	96.8	288	12	US-10-032-214-248	Sequence 248, Appl
32	1111	96.7	288	12	US-10-032-214-238	Sequence 238, Appl
33	1110	96.6	288	12	US-10-032-214-236	Sequence 236, Appl
34	1109	96.5	288	12	US-10-032-214-88	Sequence 88, Appl
35	1109	96.5	288	12	US-10-032-214-89	Sequence 89, Appl
36	1109	96.5	288	12	US-10-032-214-92	Sequence 92, Appl
37	1109	96.5	288	12	US-10-032-214-249	Sequence 249, Appl
38	1108	96.4	287	12	US-10-032-214-243	Sequence 243, Appl
39	1105	96.2	288	12	US-10-032-214-81	Sequence 81, Appl
40	1104	96.1	287	12	US-10-032-214-74	Sequence 74, Appl
41	1104	96.1	300	12	US-10-032-214-232	Sequence 232, Appl
42	1103	96.0	288	12	US-10-032-214-91	Sequence 91, Appl
43	1103	96.0	288	12	US-10-032-214-229	Sequence 229, Appl
44	1103	96.0	288	12	US-10-032-214-231	Sequence 231, Appl
45	1101	95.8	288	12	US-10-032-214-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match	100.0%	Score 1149;	DB 10;	Length 226;
Best Local Similarity	100.0%;	Pred. No. 5.1e-103;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GLSHFCSGVIHVTKEVKEVATISCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPE	60	
Db	11	GLSHFCSGVIHVTKEVKEVATISCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPE	70	
QY	61	YKNRTFIDITNNLSIVILALRSDSGTVECVLVYKVKQAFKREHLAEVTLVKADFPPTS	120	
Db	71	YKNRTFIDITNNLSIVILALRSDSGTVECVLVYKVKQAFKREHLAEVTLVKADFPPTS	130	
QY	121	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSDPEPELVAVSKLDF	180	
Db	131	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSDPEPELVAVSKLDF	190	
QY	181	NMTNHSFMCILIKYGHRLRVNQTFNNTTKQEHFPDN	216	

Db 191 NM1TNSFMCLIKYGLHURVQNTFNWNTTKQBHPDN 226
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RESULT 2
US-08-592-711-2
Sequence 2, Application US/08592711
Publication No. US20020115214A1
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
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IDENTIFICATION METHOD: sequence
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NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
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IDENTIFICATION METHOD: sequence
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IDENTIFICATION METHOD: sequence
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NAME/KEY: N-linked glycosylation
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IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
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IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
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NAME/KEY: N-linked glycosylation
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FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
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NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.

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M protein - protein search, using sw model

run on: August 26, 2003, 12:18:59 ; Search time 17 Seconds
(without alignments)
537.597 Million cell updates/sec

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effect score: 1149
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Gapop 10.0 , Gapext 0.5

searched: 328717 seqs, 42310858 residues

total number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	2	US-08-147-772-2
2	1149	100.0	288	2	US-08-456-104-6
3	1149	100.0	288	2	US-08-101-624-23
4	1149	100.0	288	2	US-08-751-767A-6
5	1149	100.0	288	3	US-08-153-262-2
6	1149	100.0	288	3	US-08-479-744A-29
7	1149	100.0	288	3	US-08-280-757B-29
8	1149	100.0	288	3	US-09-159-135-2
9	1149	100.0	288	3	US-08-205-697A-19
10	1149	100.0	288	3	US-08-702-525-19
11	1149	100.0	288	4	US-09-450-798-2
12	1149	100.0	288	4	US-08-403-253A-2
13	1149	100.0	288	4	US-09-651-200-13
14	1149	100.0	288	4	US-09-667-135-34
15	1149	100.0	288	4	US-08-435-816A-2
16	1149	100.0	288	5	PCT-US95-02576-19
17	1149	100.0	473	3	US-09-171-945-131
18	1102	95.9	208	4	US-09-460-384-36
19	1100	95.7	288	4	US-09-651-200-14
20	1050	91.4	208	3	US-08-630-172-15
21	1050	91.4	208	3	US-09-375-419-15
22	743	64.7	292	4	US-09-651-200-16
23	743	64.7	292	4	US-09-303-040-2
24	739	64.3	292	4	US-09-303-040-4
25	738	64.2	299	4	US-09-651-200-15
26	561	48.8	306	3	US-08-205-697A-17
27	561	48.8	306	3	US-08-702-525-17

28 561 48.8 306 4 US-09-651-200-17 Sequence 17, Appl
29 561 48.8 306 4 US-09-667-135-35 Sequence 35, Appl
30 561 48.8 306 5 PCT-US95-02576-17 Sequence 17, Appl
31 561 48.8 320 3 US-08-205-697A-2 Sequence 2, Appl
32 561 48.8 320 3 US-08-702-525-2 Sequence 2, Appl
33 561 48.8 320 5 PCT-US95-02576-2 Sequence 2, Appl
34 558 48.6 306 2 US-08-147-772-4 Sequence 4, Appl
35 558 48.6 306 2 US-08-456-104-8 Sequence 8, Appl
36 558 48.6 306 2 US-08-101-624-25 Sequence 25, Appl
37 558 48.6 306 3 US-08-153-262-4 Sequence 4, Appl
38 558 48.6 306 3 US-08-479-744A-31 Sequence 31, Appl
39 558 48.6 306 3 US-08-280-757B-31 Sequence 31, Appl
40 558 48.6 306 4 US-09-159-135-4 Sequence 4, Appl
41 558 48.6 306 3 US-09-450-798-4 Sequence 4, Appl
42 311 27.1 200 3 US-08-205-697A-9 Sequence 9, Appl
43 311 27.1 200 3 US-08-702-525-9 Sequence 9, Appl
44 311 27.1 200 5 PCT-US95-02576-9 Sequence 9, Appl
45 311 27.1 214 3 US-08-205-697A-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-147-772-2
; Sequence 2, Application US/08147772
; Patent No. 5858776
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: For CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	27	GLSHFCSGVIHVTKEVATLS	CGHNVSVELAOTRIYQKEKKVLTMSGDMNIWPE	86
QY	61	YKNTIFDITNLSIVILALRPS	DEGTVECVLVKEDAFKEHLAEVTLVKADFPPTS	120
Db	87	YKNTIFDITNLSIVILALRPS	DEGTVECVLVKEDAFKEHLAEVTLVKADFPPTS	146
QY	121	ISDFRPTSNIRRIICSTSGG	PPHLSWLENGEELNAINTTVSQDPETELVAVSKLDF	180
Db	147	ISDFRPTSNIRRIICSTSGG	PPHLSWLENGEELNAINTTVSQDPETELVAVSKLDF	206
QY	181	NMTNHSFCLIKYGHRLVNOT	FNNTTKQEHFPDN	216
Db	207	NMTNHSFCLIKYGHRLVNOT	FNNTTKQEHFPDN	242

RESULT 2

US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids